

Figure 1A

1	CCACTGTGCTGGAATTCGGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGG	60
61	TAAATCAGAGATCCCAAGCAAGCGCGTGCATGATAGCGAAGAAAAAAGCTATCCG	120
121	TTTCAGTTAACTACTTACCAAGATTGAATTCGCCATCGGGCAAATTACTAAAAATACAT	180
181	AAGTGCAACTCGTCCACTGTGTGTTGTGTTTTTTTTTTTTTTTGGTTTTCGCTGTGCC	240
241	TTTATCGCAAACAAGAACTGATAAACTAGAAAATATCTTGAGAACTTGTTTTTCGCGCT	300
301	TTTCTTTTGCTAATTGCCGATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTG	360
361	GTAATACAATCTGAAAAGGGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTGC	420
421	CAGCTTATCATCTCATGCTGTCTGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAAT	480
481	ACATAGAGTGTGTTTCATATAAAGTGCGACAAAGCTCGATTGGAAACAGCTGTCGAGTGCC	540
541	CTTGAGTGGGTGGGCAAGATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGC	600
601	ATCAGCATCTGGAGGCCCCGGATGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCC	660
1		3
	<u>M T A</u>	
661	GAGACCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTCCGGCCAAA	720
4	<u>E T L K P F I T P T S A N D D G F P A K</u>	23
721	GCGACCAGCACGGCGACCGCCAGCGACGACCCGCCAGCTGATCCCCCTGGTTTGGGG	780
24	<u>A T S T A T A Q R R T R Q L I P L V L G</u>	43
781	TTCATCGGTCTGGGGCTGGTTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGT	840
44	<u>F I G L G L V V A I L A L T I W Q T T R</u>	63
841	GTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAG	900
64	<u>V S H L D K E L K S L K R V V D N L Q Q</u>	83
901	CGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCC	960
84	<u>R L G I N Y L D E F D E F Q K E Y E N A</u>	103
961	CTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGC	1020
104	<u>L I D Y P K K V D G L T D E E D D D D G</u>	123

Figure 1B

1021	GATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGAT	1080
124	D G L D S I A D D E D D D V S Y S S V D	143
1081	GATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACAATGCACAT	1140
144	D V G A D Y E D Y T D M L N K L N N A H	163
1141	ACCGGCACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCA	1200
164	T G T T P T S E T T A E G E G E T D S A	183
1201	TCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTCAGATGCCCTCAAA	1260
184	S S A S N D D N V F D D F T S S D A L K	203
1261	AAGAAGCAGGAGAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATT	1320
204	K K Q E R K S R S I A D V R N E E Q N I	223
1321	CAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCCAAAGAGAGC	1380
224	Q G N H T E L Q E K S S N E A A S K E S	243
1381	CCTGCAGCACTTCACCTCCGTCGCAGAATGCATTCCCGCCATCGCCACCTCGTAGTCCGC	1440
244	P A A L H L R R R M H S R H R H L V V R	263
1441	AAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGGCGGCGT	1500
264	K A R S E D S R P A A H F H L S S R R R	283
1501	CACCAAGAAAGTATGGGCTACCATGGAGATATGTACATAGAAAATGATAGGGAGAGATGC	1560
284	H Q E S M G Y H G D M Y I E N D R E R C	303
1561	TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTATTGACGGTGACCAATGCAGGCCTA	1620
304	S Y Q G H F Q T R D G V <b>LTTAVCTNANGIL</b>	323
1621	TATTACGTATACGCCCAGATATGGGGCTACAACTCGCACGACCAGAACGGATTTATCGTC	1680
324	<b>Y:Y:V:Y:A:Q:I:W</b> G Y N S H D Q N G F I V	343
1681	TTTCAAGGAGACACTCCATTCCCTGCAGTGCTTGAACACGGTGCCCAACATGCCACAT	1740
344	F Q G D T P F L Q C L N T V P T N M P H	363
1741	AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT	1800
364	K V H T C H T S G L I H L E R N E R I H	383
1801	CTGAAGGACATTCAACAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC	1860
384	L K D I H N D R N A V L R E G N N R S Y	403

[illegible]

Figure 2A

1	ATGACTGCCGAGACCCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTT	60
1	M T A E T L K P F I T P T S A N D D G F	20
61	CCGGCCAAAGCGACCAGCACGGCGACCGCCAGCGACGACCCGCCAGCTGATCCCCCTG	120
21	P A K A T S T A T A Q R R T R Q L I P L	40
121	GTTTTGGGGTTCATCGGTCTGGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAG	180
41	V L G F I G L G L V V A I L A L T I W Q	60
181	ACAACGCGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAAT	240
61	T T R V S H L D K E L K S L K R V V D N	80
241	CTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTTCGACGAGTTCCAAAAGGAGTAC	300
81	L Q Q R L G I N Y L D E F D E F Q K E Y	100
301	GAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC	360
101	E N A L I D Y P K K V D G L T D E E D D	120
361	GACGATGGCGATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGC	420
121	D D G D G L D S I A D D E D D D V S Y S	140
421	TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAAC	480
141	S V D D V G A D Y E D Y T D M L N K L N	160
481	AATGCACATACCGGCACCACGCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACG	540
161	N A H T G T T P T S E T T A E G E G E T	180
541	GACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTACAAT	600
181	D S A S S A S N D D N V F D D F T S Y N	200
601	GCCCCAAAAAGAAGCAGGAGAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAG	660
201	A H K K K Q E R K S R S I A D V R N E E	220
661	CAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCC	720
221	Q N I Q G N H T E L Q E K S S N E A T S	240
721	AAAGAGAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGGTGAATCTCTTCTT	780
241	K E R M H S R H R H L L V R K G E S L L	260
781	TCAGCCAGATCCGAGGACTCGAGGCCAGCAGCCATTTCCACTTGAGCAGCAGGCGGCGT	840
261	S A R S E D S R P A A H F H L S S R R R	280
841	CACCAAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAAC	900
281	H Q G S M G Y H G D M Y I G N D N E R N	300

[illegible]

Figur 3A

1	GGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGGTAAATCAGAGATCCCAAG	60
61	CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTAC	120
121	CAAGATTGAATTTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT	180
181	GTGTGTTGTGTTTTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAAC	240
241	TGATAAAACTAGAAAATATCTTGAGAAACTTGTTTTTCGCGCTTTTCTTTTGCTAATTGCC	300
301	GATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG	360
361	GGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGC	420
421	TGTCTGTGAGGTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTTATA	480
481	TAAAGTGCGACAAAGCTCGATTGGAAACAGCTGTGAGTGCCCTTGAGTGGGTGGGCAAG	540
541	ATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCC	600
601	CGGTTGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCCGAGACCCCTCAAGCCGTTT	660
1	<u>M T A E T L K P F</u>	9
661	ATAACGCCAACGAGTGCCAACGATGATGGTTTTCCGGCCAAAGCGACCAGCACGGCGACC	720
10	<u>I T P T S A N D D G F P A K A T S T A T</u>	29
721	GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTTGGGGTTTCATCGGTCTGGGGCTG	780
30	<u>A Q R R T R Q L I P L V L G F I G L G L</u>	49
781	GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGTGTATCGCATCTGGACAAG	840
50	<u>V V A I L A L T I W Q T T R V S H L D K</u>	69
841	GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTAT	900
70	E L K S L K R V V D N L Q Q R L G I N Y	89
901	CTGGACGAGTTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA	960
90	L D E F D E F Q K E Y E N A L I D Y P K	109
961	AAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGATTCCATT	1020
110	K V D G L T D E E D D D D G D G L D S I	129

# Figur 3B

1021	GCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTAC	1080
130	A D D E D D D V S Y S S V D D V G A D Y	149
1081	GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCCACA	1140
150	E D Y T D M L N K L N N A H T G T T P T	169
1141	TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGAT	1200
170	S E T T A E G E G E T D S A S S A S N D	189
1201	GACAATGTGTTTCGATGACTTTACCAGCTACAATGCCACAAAAAGAAGCAGGAGAGAAAA	1260
190	D N V F D D F T S Y N A H K K K Q E R K	209
1261	TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG	1320
210	S R S I A D V R N E E Q N I Q G N H T E	229
1321	CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCACCACTTCACCAC	1380
230	L Q E K S S N E A T S K E S P A P L H H	249
1381	CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC	1440
250	R R R M H S R H R H L L V R K A R S E D	269
1441	TCGAGGCCAGCAGCCCCATTTCCACTTGAGCAGCAGGCGGCGTCACCAAGGAAGTATGGGC	1500
270	S R P A A H F H L S S R R R H Q G S M G	289
1501	TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT	1560
290	Y H G D M Y I G N D N E R N S Y Q G H F	309
1561	CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCGAG	1620
310	Q T R D G V <b>L T V T N T G L Y Y V Y A I C</b>	329
1621	ATATGCTACAACAACTCGCAGCAGGACGAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA	1680
330	<b>E Q Y</b> N N S H D Q N G F I V F Q G D T P	349
1681	TTCCTGCAGTGCTTGAACACGGTGCCACCAACATGCCACATAAGGTGCACACCTGCCAC	1740
350	F L Q C L N T V P T N M P H K V H T C H	369
1741	ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTCAACAAC	1800
370	T S G L I H L E R N E R I H L K D I H N	389
1801	GATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG	1860
390	D R N A V L R E G N N R S Y F G I F K V	409
1861	TAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTTAAGCTTTTGTCCCCG	1920

Figure 3C

1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980  
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040  
2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATA 2100  
2101 TG TAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148

1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980  
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040  
2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATA 2100  
2101 TG TAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148



Figur 4

		1	50
DmTNF	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv1	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv2	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
		51	100
DmTNF	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv1	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv2	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
		101	150
DmTNF	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDVSYSSVDDVGADYE	
DmTNFv1	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDVSYSSVDDVGADYE	
DmTNFv2	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDVSYSSVDDVGADYE	
		151	200
DmTNF	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNVDFDFTSS	
DmTNFv1	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNVDFDFTSS	
DmTNFv2	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNVDFDFTSS	
		201	250
DmTNF	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
DmTNFv1	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
DmTNFv2	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
		251	300
DmTNF	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQCSMGYHGDM	
DmTNFv1	(243)	-RMHSRHRHLVVRKGESLLSARSEDSRPAAHFHLSSRRRHQCSMGYHGDM	
DmTNFv2	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQCSMGYHGDM	
		301	350
DmTNF	(295)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICNNNSHDONGFIVE	
DmTNFv1	(292)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICNNNSHDONGFIVE	
DmTNFv2	(295)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICNNNSHDONGFIVE	
		351	400
DmTNF	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
DmTNFv1	(342)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
DmTNFv2	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
		401	415
DmTNF	(395)	LREGNNRSYFGIFKV	
DmTNFv1	(392)	LREGNNRSYFGIFKV	
DmTNFv2	(395)	LREGNNRSYFGIFKV	

## Figure 5

AC005974 : DS05033 (P1 D347), DS01913 (P1 D350). Finished; 158983 bases.  
Length = 158,983

Minus Strand HSPs:

Score = 77 (27.1 bits), Expect = 5.5, P = 1.0  
Identities = 20/58 (34%), Positives = 31/58 (53%), Frame = -1

Query: 203 NGKLIVNQDGFYYLYANICFRH-HETSGDLA----TEYLQLMVYV-TKTSIKIPSSHT 254  
+G L V G YY+YA IC+ + H+ +G + T +LQ + V T K+ + HT  
Sbjct: 129394 DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHT  
129221

Score = 45 (15.8 bits), Expect = 79., Sum P(2) = 1.0  
Identities = 9/17 (52%), Positives = 10/17 (58%), Frame = -1

Query: 28 GPLHAPP--PPAPHQPP 42  
GP PP PP+P PP  
Sbjct: 132361 GPSLPPFPFPPSPRTTP 132311

129394 DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHT  
129221

Figure 6A

		1		50
DmTNF	(1)	--MTAETLKPFITPTTSANDDCFFAKATSTATAQR-----		
DmTNFv1	(1)	--MTAETLKPFITPTTSANDDCFFAKATSTATAQR-----		
DmTNFv2	(1)	--MTAETLKPFITPTTSANDDCFFAKATSTATAQR-----		
Osteoprotegerin	(1)	-----MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAP		
hCD27L	(1)	-----		
hCD30L	(1)	-----		
hTRAIL	(1)	-----MAMMEVOEGP-----		
hEctodysplasmin_A	(1)	MGYPEVERRELTPAAAPRPRCSQCCGCGAPARA-----		
mEctodysplasmin_A	(1)	MGYPEVERREPTPAAAPRPRCSQCCGCRGAPARA-----		
		51		100
DmTNF	(33)	----RTRQLIPVLGFIGLGLVVAHLALTIWQTRVSHLDKELKSLKRVV		
DmTNFv1	(33)	----RTRQLIPVLGFIGLGLVVAHLALTIWQTRVSHLDKELKSLKRVV		
DmTNFv2	(33)	----RTRQLIPVLGFIGLGLVVAHLALTIWQTRVSHLDKELKSLKRVV		
Osteoprotegerin	(39)	HQPPAASRSMFVALLGLGLGVVCSVALFFMFRAQMDPN-----RISE		
hCD27L	(1)	-----		
hCD30L	(1)	-----		
hTRAIL	(11)	----SLGQTCVLIIVITVQLQSLCAVTVVFTNEI-----KOMQ		
hEctodysplasmin_A	(35)	----GEGNSCLIFLGFGLSLAHHLITLCCMLELRS-----ELRRER		
mEctodysplasmin_A	(35)	----GEGNSCLIFLGFGLSLAHHLITLCCMLELRS-----ELRRER		
		101		150
DmTNF	(79)	DNLQQRLLGINYLDEFDEFQKEYENALIDYPKKVDCLTDIEDDDDGDGLDS		
DmTNFv1	(79)	DNLQQRLLGINYLDEFDEFQKEYENALIDYPKKVDCLTDIEDDDDGDGLDS		
DmTNFv2	(79)	DNLQQRLLGINYLDEFDEFQKEYENALIDYPKKVDCLTDIEDDDDGDGLDS		
Osteoprotegerin	(82)	DGTHCIYR-----ILRLHENAQFQDTTLESQDT---		
hCD27L	(1)	-----		
hCD30L	(1)	-----		
hTRAIL	(47)	DKYSKS---G-----IACFLKEDDSYWPNDDES---		
hEctodysplasmin_A	(73)	GAESRLCGSGTPTGSGTLSSLGGLDPDSPITSHLCQPSPKQPLEPGEAA		
mEctodysplasmin_A	(73)	GTESRLCGPGAPGSGTLSSPGSLDPVGPITRHLQPSFQQQPLEPGEEDP		
		151		200
DmTNF	(129)	IADDEDIDVSYSSVDDVGADYEDYEDMLNKLNNAHIGTTPTSETTAEGEG		
DmTNFv1	(129)	IADDEDIDVSYSSVDDVGADYEDYEDMLNKLNNAHIGTTPTSETTAEGEG		
DmTNFv2	(129)	IADDEDIDVSYSSVDDVGADYEDYEDMLNKLNNAHIGTTPTSETTAEGEG		
Osteoprotegerin	(110)	-----KLIPDSCRRIKQAFQGAQVQELQHIVGSQHIRAE		
hCD27L	(1)	-----MPEEGSGCSVRPRPYGCVLRAALVPL		
hCD30L	(1)	-----MDPCLQALNGMAPPGDTAMHVPAGSVAS		
hTRAIL	(73)	-----MN--SPCQVQVQLRQLVRKMLIRTSEETISTVQ		
hEctodysplasmin_A	(123)	IHSDSQDGHQMALINFFFPDEKPYSEESRR--VRNKRKSKSNEGADGCPV		
mEctodysplasmin_A	(123)	IPPDSQDRHQMALINFFFPDEKAYSEESRR--VRNKRKSKSGEGADGCPV		
		201		250
DmTNF	(179)	ETD-SASSASNDNVFDDFTSSDALKKKQERKRSSTADVRNEEQNTQCNH		
DmTNFv1	(179)	ETD-SASSASNDNVFDDFTSYNAHKKKQERKRSSTADVRNEEQNTQCNH		
DmTNFv2	(179)	ETD-SASSASNDNVFDDFTSYNAHKKKQERKRSSTADVRNEEQNTQCNH		
Osteoprotegerin	(144)	KAMVDG-----SWLDIAK-----		
hCD27L	(27)	VAG-----LVICLVVCLQR-----		
hCD30L	(30)	HLGTTSRSYFYLTATLALCLVFTVATIMVLVVQRTDSTPN-----		
hTRAIL	(105)	EKQQ-----NISPLVR-----		
hEctodysplasmin_A	(171)	KNK-KKGKKA GPPGPNPPGPPGPPGPPGPPGIPGTPGPG--TTVMGPP		
mEctodysplasmin_A	(171)	KNK-KKGKKA GPPGPNPPGPPGPPGPPGPPGIPGTPGPG--TTVMGPP		
		251		300
DmTNF	(228)	TELQEKSSNEAASKESPAALHLRRRMHSRHRHLVVRK-----ARSEDNR		
DmTNFv1	(228)	TELQEKSSNEATSKE-----RMHSRHRHLVVRKGESLLSARSEDNR		
DmTNFv2	(228)	TELQEKSSNEATSKEAPLHRRRMHSRHRHLVVRK-----ARSEDNR		
Osteoprotegerin	(157)	-----RSKLEAQP-----		
hCD27L	(41)	-----FAQAAQQLPLES-----		
hCD30L	(71)	-----SDNVPLKCGN-----CSED		
hTRAIL	(116)	-----ERGPQ-----RVAAHITGTR-----		
hEctodysplasmin_A	(218)	GPPGPPGPQGPPGLQGP-----SGAADKACTR-----ENQP		
mEctodysplasmin_A	(218)	GPPGPPGPQGPPGLQGP-----SGAADKTGTR-----ENQP		

Figur 6B

		301		350
DmTNF	(272)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-CSYQGHQOTRDGVLTVTN		
DmTNFv1	(269)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-NSYQGHQOTRDGVLTVTN		
DmTNFv2	(272)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-NSYQGHQOTRDGVLTVTN		
Osteoprotegerin	(165)	--FAHLTINATDIPSG-SHKVSLSSWYHARG-WAKELSNMTFSNCKLIVNQ		
hCD27L	(53)	--LGWDVDELQLNHTGPPQDPRIYWQGGPALGRSELHGPELDKCOLRTHR		
hCD30L	(86)	LLCILKRAPPFKKSWAYLQVAKHINKTKLSWNKDELLHGVRYPQDGNLVITQF		
hTRAIL	(131)	-GRSN-TLSSPNSKNEKALGRKINSWESSRSGHSFLSMHLRNGELVITHE		
hEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNDLSGGLNDWSRITM-NEKMFKLHPRSGELEVLV		
mEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNDLSGGLNDWSRITM-NEKMFKLHPRSGELEVLV		
		351		400
DmTNF	(321)	AGLYYYVY-----AQHWGYNSHDONGEIVEFG-ETPFLOCLNTVPTNM		
DmTNFv1	(318)	TGLYYVYVY-----AQHCYNNSHDONGEIVEFG-ETPFLOCLNTVPTNM		
DmTNFv2	(321)	TGLYYVYVY-----AQHCYNNSHDONGEIVEFG-ETPFLOCLNTVPTNM		
Osteoprotegerin	(211)	DGFYYEYANICFRHHETSGDLATEYLLQLMVYVTKTSIKHPSSTHLMKGGGS		
hCD27L	(101)	DGLYMMVHTQVTLAICSSHTASRHHPTLLAVGHCSS--PASRSISLERLSF		
hCD30L	(136)	PCLYFTICQLQFLVQCPNNSVDLKLLELLINKHIKKQALVTVCESGMOTKH		
hTRAIL	(179)	KGEYYHYSCQTYFRFQEEIKENIKNDKQMVQYHYK-YTSYPPPLLLMK SAR		
hEctodysplasmin_A	(298)	DGTVEHYYSQ-----VEVYYINFTDFASVEVVVD-EKPFLOCTRSTETGK		
mEctodysplasmin_A	(298)	DGTVEHYYSQ-----VEVYYINFTDFASVEVVVD-EKPFLOCTRSTETGK		
		401		450
DmTNF	(362)	PHK-----VHTCHTSGLIHLEARNERITHKDI-INRNAVIREGNNRSY		
DmTNFv1	(359)	PHK-----VHTCHTSGLIHLEARNERITHKDI-INRNAVIREGNNRSY		
DmTNFv2	(362)	PHK-----VHTCHTSGLIHLEARNERITHKDI-INRNAVIREGNNRSY		
Osteoprotegerin	(261)	TKYWSGNSEPHFYSINVCGEFKLSCEETISTEVSNPSTLDPDQ---DAFY		
hCD27L	(148)	HQG-----CTIVSORLTPLARGDTLCTNLGTLLPSRNT---DETF		
hCD30L	(186)	VYQN-----LSQFLDYLLQVNTTISVNVDTFYIDTSTFPLENVL		
hTRAIL	(228)	NSCWSKDAEYGLYSIYQCCIFELKENDRIFVSVTNEHLIDMDH---EASE		
hEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTF		
mEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTF		
		451		462
DmTNF	(404)	FGIFKV-----		
DmTNFv1	(401)	FGIFKV-----		
DmTNFv2	(404)	FGIFKV-----		
Osteoprotegerin	(308)	FGAFKVRDID--		
hCD27L	(186)	FGVQWVRP----		
hCD30L	(226)	SIFYSNSD----		
hTRAIL	(275)	FGAFLVG----		
hEctodysplasmin_A	(380)	FGAFLRGEAPAS		
mEctodysplasmin_A	(380)	FGAFLRGEAPAS		

Figure 7

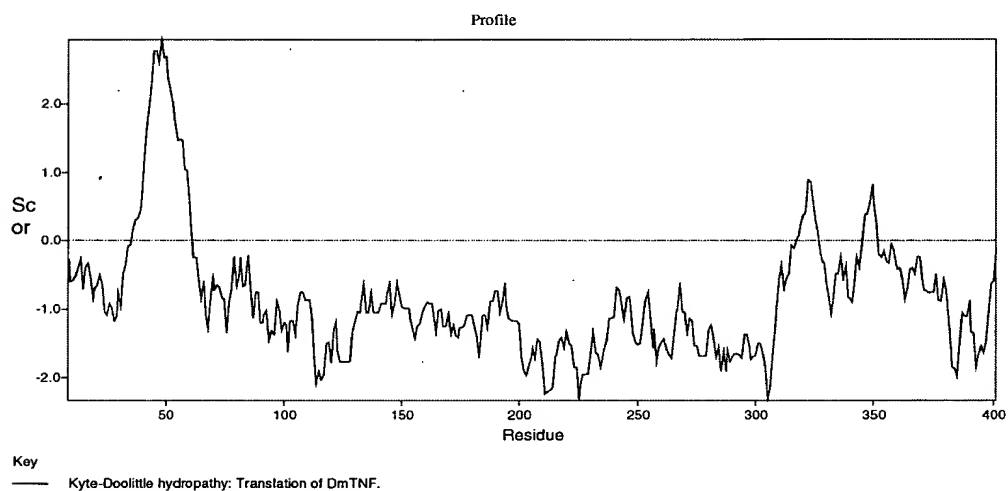


Figure 8

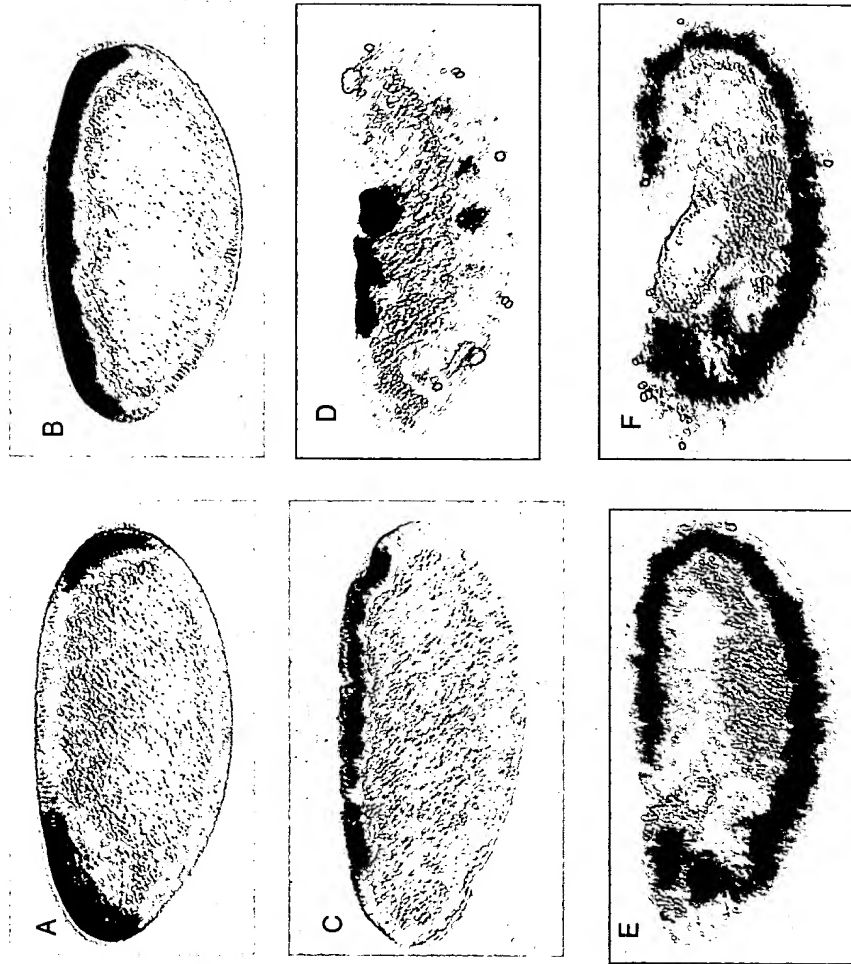


Figure 9

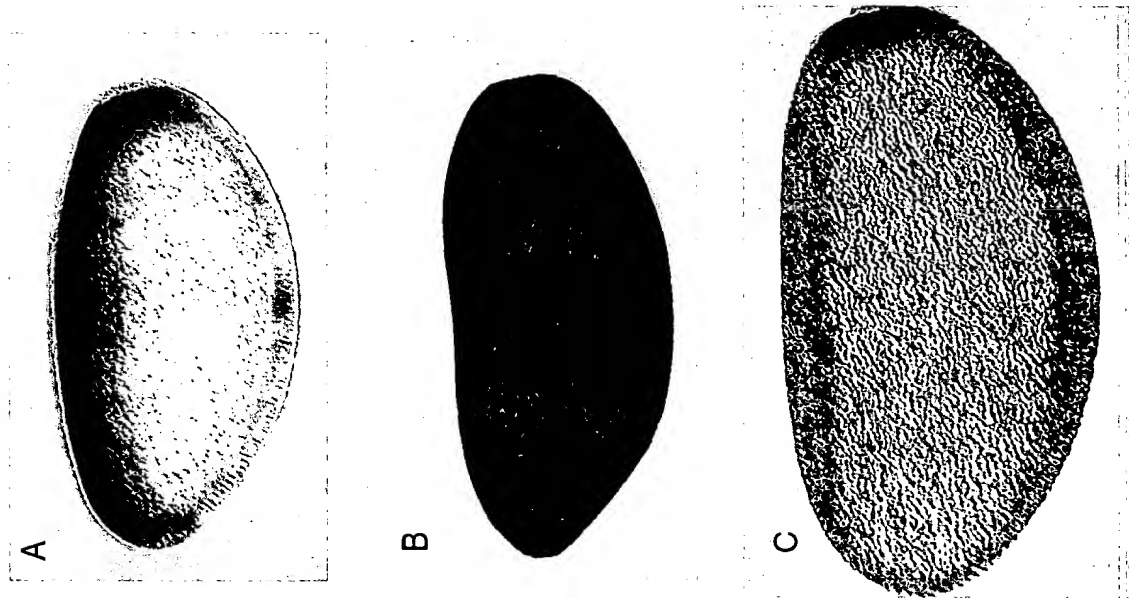


Figure 10

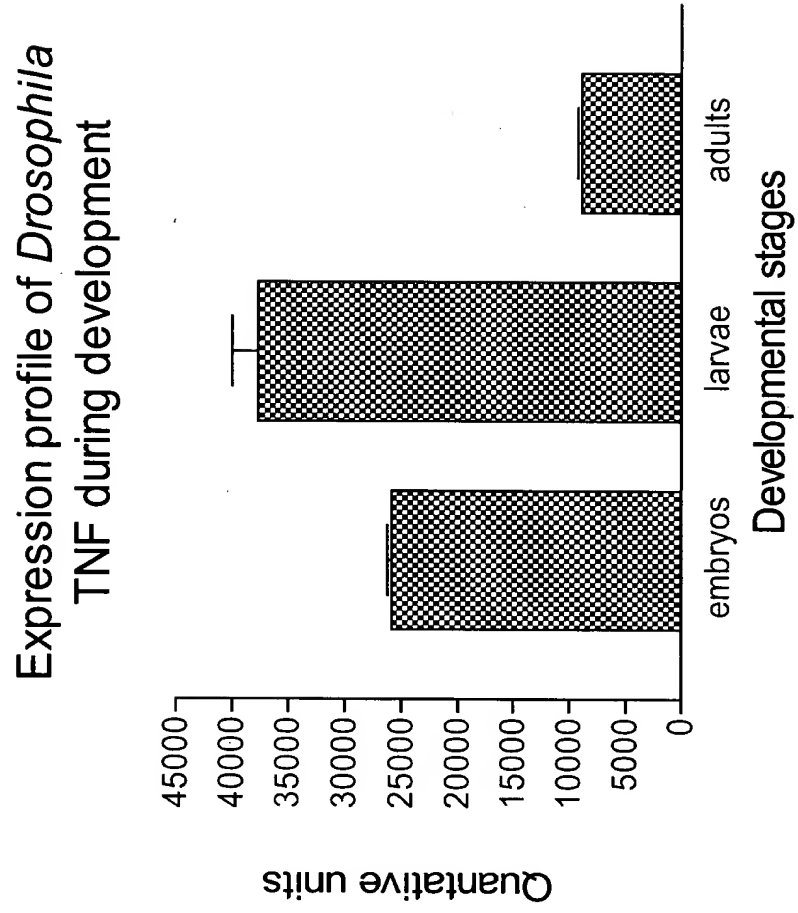




Figure 11

**DmTNF**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.6%	34.4%
human ectodysplasmin_A protein	gilQ92838	21.2%	27.9%
mouse ectodysplasmin_A protein	gilNP_034229	20.4%	28.5%

**DmTNFv1**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	23.8%	30.5%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	23.3%	32.7%
human ectodysplasmin_A protein	gilQ92838	21.8%	28.6%
mouse ectodysplasmin_A protein	gilNP_034229	21%	28.6%

**DmTNFv2**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.1%	33.9%
human ectodysplasmin_A protein	gilQ92838	22.4%	29.1%
mouse ectodysplasmin_A protein	gilNP_034229	21.6%	29.2%

Figure 12

S-dmTNF

